

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Collins, Mary
Donaldson, Debra
Fitz, Lori
Neben, Tamlyn
Whitters, Matthew
Wood, Clive
- (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: GI5268
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 256..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG	60
CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA	120
AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAGGA GGACAAAGAG GTCTTGTGAT	180
AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA	240
CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT	291
Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile	
1 5 10	
CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT	339
Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro	
15 20 25	
CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT	387
Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr	
30 35 40	
TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA	435
Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr	
45 50 55 60	
CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG	483
Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys	
65 70 75	
ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT	531
Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn	
80 85 90	
AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA	579
Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr	
95 100 105	
AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA	627
Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile	
110 115 120	
TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA	675
Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile	
125 130 135 140	
TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA	723

Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Lys	Thr		
				145					150					155			
GTA	TAT	TCT	GAT	ACC	AAC	TAT	ACC	ATG	TTT	TTC	TGG	TAT	GAG	GGC	TTG	771	
Val	Tyr	Ser	Asp	Thr	Asn	Tyr	Thr	Met	Phe	Phe	Trp	Tyr	Glu	Gly	Leu		
			160					165					170				
GAT	CAT	GCC	TTA	CAG	TGT	GCT	GAT	TAC	CTC	CAG	CAT	GAT	GAA	AAA	AAT	819	
Asp	His	Ala	Leu	Gln	Cys	Ala	Asp	Tyr	Leu	Gln	His	Asp	Glu	Lys	Asn		
		175					180					185					
GTT	GGA	TGC	AAA	CTG	TCC	AAC	TTG	GAC	TCA	TCA	GAC	TAT	AAA	GAT	TTT	867	
Val	Gly	Cys	Lys	Leu	Ser	Asn	Leu	Asp	Ser	Ser	Asp	Tyr	Lys	Asp	Phe		
	190					195					200						
TTT	ATC	TGT	GTT	AAT	GGA	TCT	TCA	AAG	TTG	GAA	CCC	ATC	AGA	TCC	AGC	915	
Phe	Ile	Cys	Val	Asn	Gly	Ser	Ser	Lys	Leu	Glu	Pro	Ile	Arg	Ser	Ser		
205				210					215					220			
TAT	ACA	GTT	TTT	CAA	CTT	CAA	AAT	ATA	GTT	AAA	CCA	TTG	CCA	CCA	GAA	963	
Tyr	Thr	Val	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro	Pro	Glu		
				225				230					235				
TTC	CTT	CAT	ATT	AGA	GTG	GAG	AAT	TCC	ATT	GAT	ATT	AGA	ATG	AAA	TGG	1011	
Phe	Leu	His	Ile	Ser	Val	Glu	Asn	Ser	Ile	Asp	Ile	Arg	Met	Lys	Trp		
			240					245				250					
AGC	ACA	CCT	GGA	GGA	CCC	ATT	CCA	CCA	AGG	TGT	TAC	ACT	TAT	GAA	ATT	1059	
Ser	Thr	Pro	Gly	Gly	Pro	Ile	Pro	Pro	Arg	Cys	Tyr	Thr	Tyr	Glu	Ile		
		255				260						265					
GTG	ATC	CGA	GAA	GAC	GAT	ATT	TCC	TGG	GAG	TCT	GCC	ACA	GAC	AAA	AAC	1107	
Val	Ile	Arg	Glu	Asp	Asp	Ile	Ser	Trp	Glu	Ser	Ala	Thr	Asp	Lys	Asn		
	270					275					280						
GAT	ATG	AAG	TTG	AAG	AGG	AGA	GCA	AAT	GAA	AGT	GAA	GAC	CTA	TGC	TTT	1155	
Asp	Met	Lys	Leu	Lys	Arg	Arg	Ala	Asn	Glu	Ser	Glu	Asp	Leu	Cys	Phe		
285					290				295					300			
TTT	GTA	AGA	TGT	AAG	GTC	AAT	ATA	TAT	TGT	GCA	GAT	GAT	GGA	ATT	TGG	1203	
Phe	Val	Arg	Cys	Lys	Val	Asn	Ile	Tyr	Cys	Ala	Asp	Asp	Gly	Ile	Trp		
				305				310					315				
AGC	GAA	TGG	AGT	GAA	GAG	GAA	TGT	TGG	GAA	GGT	TAC	ACA	GGG	CCA	GAC	1251	
Ser	Glu	Trp	Ser	Glu	Glu	Glu	Cys	Trp	Glu	Gly	Tyr	Thr	Gly	Pro	Asp		
			320				325						330				
TCA	AAG	ATT	ATT	TTC	ATA	GTA	CCA	GTT	TGT	CTT	TTC	TTT	ATA	TTC	CTT	1299	
Ser	Lys	Ile	Ile	Phe	Ile	Val	Pro	Val	Cys	Leu	Phe	Phe	Ile	Phe	Leu		
		335				340					345						
TTG	TTA	CTT	CTT	TGC	CTT	ATT	GTG	GAG	AAG	GAA	GAA	CCT	GAA	CCC	ACA	1347	
Leu	Leu	Leu	Leu	Cys	Leu	Ile	Val	Glu	Lys	Glu	Pro	Glu	Pro	Thr			
	350					355					360						

TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT 1395
 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
 365 370 375 380

ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG 1444
 Thr Leu Cys

TCATATTAAA CTCAATTCTCT CTTAAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA 1504

AAAAAAAAAA AAAA ACTCGA G 1525

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Phe	Val	His	Ile	Arg	Cys	Leu	Cys	Phe	Ile	Leu	Leu	Cys	Thr	
1				5				10						15		
Ile	Thr	Gly	Tyr	Ser	Leu	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	
			20					25						30		
Glu	Ile	Leu	Asp	Pro	Gly	Leu	Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Lys	
			35				40						45			
Pro	Pro	Val	Val	Ile	Glu	Lys	Phe	Lys	Gly	Cys	Thr	Leu	Glu	Tyr	Glu	
			50				55					60				
Leu	Lys	Tyr	Arg	Asn	Val	Asp	Ser	Asp	Ser	Trp	Lys	Thr	Ile	Ile	Thr	
			65			70				75					80	
Arg	Asn	Leu	Ile	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	
					85					90				95		
Gly	Lys	Ile	Arg	Thr	His	Leu	Ser	Glu	His	Cys	Thr	Asn	Gly	Ser	Glu	
					100			105					110			
Val	Gln	Ser	Pro	Trp	Ile	Glu	Ala	Ser	Tyr	Gly	Ile	Ser	Asp	Glu	Gly	
			115				120						125			
Ser	Leu	Glu	Thr	Lys	Ile	Gln	Asp	Met	Lys	Cys	Ile	Tyr	Tyr	Asn	Trp	
			130				135					140				
Gln	Tyr	Leu	Val	Cys	Ser	Trp	Lys	Pro	Gly	Lys	Thr	Val	Tyr	Ser	Asp	
			145				150				155				160	
Thr	Asn	Tyr	Thr	Met	Phe	Phe	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	

165										170					175				
Gln	Cys	Ala	Asp	Tyr	Leu	Gln	His	Asp	Glu	Lys	Asn	Val	Gly	Cys	Lys				
			180					185					190						
Leu	Ser	Asn	Leu	Asp	Ser	Ser	Asp	Tyr	Lys	Asp	Phe	Phe	Ile	Cys	Val				
		195					200					205							
Asn	Gly	Ser	Ser	Lys	Leu	Glu	Pro	Ile	Arg	Ser	Ser	Tyr	Thr	Val	Phe				
	210					215					220								
Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro	Pro	Glu	Phe	Leu	His	Ile				
225				230					235					240					
Ser	Val	Glu	Asn	Ser	Ile	Asp	Ile	Arg	Met	Lys	Trp	Ser	Thr	Pro	Gly				
			245					250						255					
Gly	Pro	Ile	Pro	Pro	Arg	Cys	Tyr	Thr	Tyr	Glu	Ile	Val	Ile	Arg	Glu				
		260					265						270						
Asp	Asp	Ile	Ser	Trp	Glu	Ser	Ala	Thr	Asp	Lys	Asn	Asp	Met	Lys	Leu				
	275					280						285							
Lys	Arg	Arg	Ala	Asn	Glu	Ser	Glu	Asp	Leu	Cys	Phe	Phe	Val	Arg	Cys				
290					295					300									
Lys	Val	Asn	Ile	Tyr	Cys	Ala	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser				
305			310						315					320					
Glu	Glu	Glu	Cys	Trp	Glu	Gly	Tyr	Thr	Gly	Pro	Asp	Ser	Lys	Ile	Ile				
			325					330						335					
Phe	Ile	Val	Pro	Val	Cys	Leu	Phe	Phe	Ile	Phe	Leu	Leu	Leu	Leu	Leu				
		340					345						350						
Cys	Leu	Ile	Val	Glu	Lys	Glu	Glu	Pro	Glu	Pro	Thr	Leu	Ser	Leu	His				
	355					360					365								
Val	Asp	Leu	Asn	Lys	Glu	Val	Cys	Ala	Tyr	Glu	Asp	Thr	Leu	Cys					
	370				375					380									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 103..1245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC	60
GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC GTT	114
Met Ala Phe Val	
1	
TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT	162
Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe	
5 10 15 20	
GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG	210
Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln	
25 30 35	
GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA	258
Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln	
40 45 50	
TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA	306
Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu	
55 60 65	
TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC	354
Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile	
70 75 80	
ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC	402
Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly	
85 90 95 100	
ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA	450
Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly	
105 110 115	
TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA	498
Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro	
120 125 130	
CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC	546
Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr	
135 140 145	
AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT	594
Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu	
150 155 160	
CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT	642
Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His	
165 170 175 180	

GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA	690
Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly	
185 190 195	
TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT	738
Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile	
200 205 210	
TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC	786
Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe	
215 220 225	
ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT	834
Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu	
230 235 240	
ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA	882
Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile	
245 250 255 260	
CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC	930
Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile	
265 270 275	
AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA	978
Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr	
280 285 290	
TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA	1026
Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val	
295 300 305	
AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG	1074
Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu	
310 315 320	
TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT	1122
Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr	
325 330 335 340	
TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA	1170
Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile	
345 350 355	
TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG	1218
Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met	
360 365 370	
ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTTCCA TATCAAGAGA	1265
Ile Pro Glu Phe Phe Cys Asp Thr *	
375 380	
CATGGTATTG ACTCAACAGT TTCCAGTCAT GGCCAAATGT TCAATATGAG TCTCAATAAA	1325
CTGAATTTTT CTTGCGAAAA AAAAAAAAAA AAATCCGCGG ATCC	1369

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
85 90 95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro

225 230 235 240
 Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
 245 250 255
 Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
 260 265 270
 Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
 275 280 285
 Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
 290 295 300
 Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
 305 310 315 320
 Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
 325 330 335
 Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
 340 345 350
 Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
 355 360 365
 Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr *
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

KSRCTCCABK CRCTCCA

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAGTTAAAC CATTGCCACC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCCATTCGC TCCAAATTCC

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTCTATCTT ACTTTTACTC G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATCTGAGCA ATAAATATTC AC

22